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OM protein - protein search, using sw model

Run on: August 21, 2002, 15:25:51 ; Search time 29.23 Seconds

(without alignments)
34.200 Million cell updates/sec

Title: US-09-633-364-6827

Perfect score: 1 VLAKELKRV 9

Sequence: BLOSUM62

Scoring table: Gapop 10.0, Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 194182

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1980.DAT:*
2: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1981.DAT:*
3: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1982.DAT:*
4: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1983.DAT:*
5: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1984.DAT:*
6: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1985.DAT:*
7: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1986.DAT:*
8: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1987.DAT:*
9: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1988.DAT:*
10: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1989.DAT:*
11: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1990.DAT:*
12: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1991.DAT:*
13: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1992.DAT:*
14: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1993.DAT:*
15: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1994.DAT:*
16: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1995.DAT:*
17: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1996.DAT:*
18: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1997.DAT:*
19: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1998.DAT:*
20: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA1999.DAT:*
21: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2000.DAT:*
22: /SIDSI/gcgdata/hold-geneseq/geneseqp-emb1/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	41	100.0	9	15	AA73864
2	41	100.0	9	21	AA72836
3	41	100.0	9	22	AAU06387
4	41	100.0	9	22	AAU06424
5	41	100.0	10	22	AAU06426
6	41	100.0	11	22	AAU06425
7	38	92.7	10	22	AAU06423
8	37	90.2	9	22	AAU06372
9	31	75.6	9	20	AA446778
10	31	75.6	15	17	AAW05203
11	28	68.3	8	12	AA14165

12	27	65.9	8	19	AAW69677	Helicobacter pylori
13	27	65.9	14	20	AAZ28976	Antimicrobial pept
14	27	65.9	14	20	AAZ28967	Antimicrobial pept
15	27	65.9	14	21	AAZ13937	Type 1 antiviral p
16	27	65.9	14	21	AAZ13946	Antiviral peptide
17	27	65.9	14	21	AAZ77081	Antimicrobial pept
18	27	65.9	14	21	AAZ77090	Antifungal peptide
19	27	65.9	14	21	AAZ50850	Antimicrobial pept
20	27	65.9	14	21	AAZ50859	Antifungal peptide
21	27	65.9	14	21	AAZ50864	Antifungal peptide
22	27	65.9	14	22	AAU07797	Human histatin 5 c
23	27	65.9	15	20	AAZ28981	Antimicrobial pept
24	27	65.9	15	21	AAZ77095	Antimicrobial pept
25	27	63.4	10	15	AAZ64030	Haematopoiesis inh
26	25	61.0	8	21	AAZ68620	Amnio acid sequenc
27	25	61.0	14	22	AAU00147	Human protein frag
28	25	61.0	14	22	AAU00148	Human protein frag
29	25	61.0	14	22	AAU00149	Human protein frag
30	24	58.5	8	12	AAZ13462	pe-GLI246, 247, 24
31	24	58.5	9	22	AAZ69052	Pseudomonas aerugi
32	24	58.5	8	22	AAZ68693	Immunogenic peptid
33	24	58.5	12	17	AAZ40659	Immunogenic peptid
34	24	58.5	14	22	AAZ97177	Human saliva protei
35	24	58.5	14	22	AAZ86894	Human peptide #43
36	23	56.1	5	17	AAZ86894	Allergen Alt a 43
37	23	56.1	7	18	AAZ31013	Timothy grass poll
38	23	56.1	7	22	AAZ46502	HLI binding site c
39	23	56.1	9	22	AAU06378	Human Leukocyte An
40	23	56.1	10	22	AAZ68588	Saccharomyces cere
41	23	56.1	14	20	AAZ28973	Antimicrobial pept
42	23	56.1	14	21	AAZ13943	Type 1 antiviral p
43	23	56.1	14	21	AAZ77087	Antimicrobial pept
44	23	56.1	14	21	AAZ50856	Antifungal peptide
45	23	56.1	14	21	AAZ50865	Antifungal peptide

ALIGNMENTS

RESULT 1

ID AAR73864 standard; peptide; 9 AA.

AA73864:

22-JUN-1995 (first entry)

Antigen fragment 180, from PAP has binding affinity for HLA-2.1.

antigen; epitope; immunogenic target protein; PSK; HBVC; EBV;

HLVI; plasma specific antigen; hepatitis B virus; Epstein Barr;

human immunodeficiency virus; human papilloma virus; p53; c-erbB2;

WAGE-1; melanoma antigen; in vivo; ex vivo; therapeutic;

pharmaceutical composition; major histocompatibility complex;

diagnostic; MHC class I molecule; major histocompatibility complex;

HLA-A2.1; gmer; Imer; anchor; human leukocyte antigen; PLP; dmer;

algorithm prediction; MBP; CMV; cytomegalovirus; HSV;

herpes simplex virus; influenza A; M1; LCMV; PAP.

OS Synthetic.

XX WO9420127-A.

XX 15-SEP-1994.

XX 04-MAR-1994; 94WO-US02353.

XX 05-MAR-1993; 93US-0027146.

XX 04-JUN-1993; 93US-0073205.

XX 29-NOV-1993; 93US-0159184.

XX (CYTE-) CYTEL CORP.

PI Grey HM, Kast WM, Sette A, Sidney J;
 XX WPI; 1994-302678/37.
 XX Immunogenic peptide(s) having an HLA-A2.1 binding motif - used
 PT for treatment or prophylaxis of cancer, virus infection or
 PT autoimmune diseases.
 XX
 XX Disclosure; Page 87; 138pp; English.
 XX AAR73685-876 are potential peptide binders of HLA-A2.1 motif. Using
 CC motifs disclosed in the invention, these peptides were screened for
 CC further motifs. Only peptides with binding affinity of at least 18
 CC (binding affinity is expressed as an IC50 value) as compared to the
 CC standard peptide (AAR71293) in assays. This peptide from PAP (SIC) has a
 CC binding value of 0.0590. The peptides of the invention can induce
 CC cytotoxic T lymphocytes which can react with target cells. They can
 CC be used for the treatment or prophylaxis of cancer, eg. prostate
 CC cancer or lymphoma, etc.
 CC
 XX Sequence 9 AA:
 SQ
 Query Match 100.0%; Score 41; DB 15; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLAKEIKFV 9
 DB 1 vlakeikfv 9
 RESULT 2
 ID AAY82836 standard; peptide: 9 AA.
 XX AAY82836;
 XX 19-JUN-2000 (first entry)
 DE Prostate acid phosphatase fragment (tumour associated antigen).
 XX
 XX Tumour associated antigen peptide; TAA; cancer; carcinoma;
 KW treatment; prevention; cure; anti-tumour vaccine; metastases;
 KW breast; bladder; prostate; pancreas; ovary; thyroid; colon;
 KW stomach; carcinoma; MHC Class I; HLA-A2; human;
 KW Major histocompatibility Complex; uroplakin;
 KW prostate specific antigen; prostate specific membrane antigen;
 KW prostate acid phosphatase; mucin; lactadherin;
 KW teratocarcinoma derived growth factor; PSA; PSMA; PAP; CRIPTO-1.
 XX
 XX Homo sapiens.
 OS
 XX MO200006723-A1.
 XX
 XX 10-FEB-2000.
 PD
 XX 29-JUL-1999; 99MO-IL00417.
 PF
 XX 30-JUL-1998; 98IL-0125608.
 PR
 XX (YEDA) YEDA RES & DEV CO LTD.
 PA (BLOT-) BIO-TECHNOLOGY GEN CORP.
 XX
 XX Eisenbach L, Garmon L, Tirosh B, Bar-naim E, Paz A, Fridkin M;
 PI Filzer-atlas C;
 XX
 XX WPI; 2000-205463/18.
 DR
 XX Tumour associated antigen peptides, especially derived from uroplakin,
 PT useful as vaccines to prevent or cure cancers including breast,
 PT bladder, prostate, pancreas, ovary, thyroid, colon and stomach -
 XX

PS Claim 10; Page 98; 113pp; English.
 XX
 XX Tumour associated antigen peptides (TAA) may be used for the
 CC treatment, prevention and cure of cancer or cancer metastases. The
 CC cancer may be breast, bladder, prostate, pancreas, ovary, thyroid,
 CC colon, stomach, head or neck cancer or a carcinoma. The tumour
 CC associated antigens are presentable to the immune system by HLA-A2
 CC molecules and are generally between 8 to 10 amino acids in length.
 CC The amino acids located at positions 2 and 9 of the tumour associated
 CC antigens are the anchor residues which participate in the binding to
 CC MHC class I molecules, more specifically HLA-A2. More tumour
 CC associated antigens are described in records AAY82806-Y82807.
 CC Those tumour associated antigens described in records AAY82806-Y82824
 CC and AAY82855-Y82869 are derived from uroplakin, such as Uroplakin II,
 CC Uroplakin Ia, Uroplakin III and Uroplakin Ib. Those described in
 CC records AAY82825-Y82829 are derived from prostate specific antigen
 CC (PSA). Those described in records AAY82830-Y82835 are derived from
 CC prostate specific membrane antigen (PSMA). Those described in
 CC records Y82836-AAY82839 are derived from prostate acid phosphatase
 CC (PAP). Those described in records AAY82840-Y82846 are derived
 CC from lactadherin (Ba-46). Those described in records AAY82847-Y82854
 CC are derived from Mucin and those described in records AAY82871-Y82882
 CC are derived from Teratocarcinoma derived growth factor (CRIPTO-1).
 CC
 XX Sequence 9 AA:
 SQ
 Query Match 100.0%; Score 41; DB 21; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VLAKEIKFV 9
 DB 1 vlakeikfv 9
 RESULT 3
 ID AAU06387 standard; peptide: 9 AA.
 XX AAU06387;
 XX 24-OCT-2001 (first entry)
 DE Human prostate antigen binding peptide #9.
 XX
 XX Prostate cancer-associated antigen; supermotif; human leukocyte antigen;
 KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;
 KW Immunogenicity; immunosuppression; HTL.
 KW
 XX Homo sapiens.
 OS
 XX MO200145728-A2.
 XX
 XX 28-JUN-2001.
 PD
 XX 20-DEC-2000; 2000MO-US35516.
 PE
 XX 21-DEC-1999; 99US-0171312.
 PR
 XX 07-AUG-2000; 2000US-0633364.
 PR
 XX (EPIM-) EPIMUNE INC.
 XX
 XX Pikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 PI Keogh E;
 XX
 XX WPI; 2001-396311/42.
 DR
 XX Tumour antigen-associated group-based vaccines useful for vaccinating
 PT against prostate cancer -
 PT Example 2; Page 237; 252pp; English.
 PS
 XX

SQ Sequence 10 AA:

Query Match 100.0%; Score 41; DB 22; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.051;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLAKELKFV 9
 :|||||
 Db 1 vlakelkf 9

RESULT 6

AAU06425 standard; Peptide: 11 AA.
 ID AAU06425

AC AAU06425;

DT 24-OCT-2001 (first entry)

DE Human Leukocyte Antigen-A2 (HLA-A2) supermotif binding peptide #17.

KW Prostate cancer-associated antigen: supermotif; human leukocyte antigen;

KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;

KW Immunogenicity; immunosuppression; HTL.

OS Homo sapiens.

PN WO200145728-A2.

PD 28-JUN-2001.

PF 20-DEC-2000; 2000WO-US35516.

PR 21-DEC-1999; 99US-0171312.

PR 07-AUG-2000; 2000US-0633364.

XX (EPIM-) EPIMUNE INC.

XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;

PI Keogh E;

PT WPI: 2001-398311/42.

PT Tumour antigen-associated group-based vaccines useful for vaccinating

PT against prostate cancer -

PS Example 2; Page 238; 252pp; English.

CC The sequences represent prostate cancer-associated antigens and derived

CC motif or supermotif epitopes. The peptide epitopes are included in

CC prostate cancer vaccine compositions due to their ability to bind to

CC human leukocyte antigen (HLA) molecules, which recognise the motifs.

CC Peptides with a high binding affinity are further tested for their

CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte

CC (HTL) response. Supermotif-bearing peptides may also be tested for their

CC binding affinity to multiple alleles within the HLA superfamily. The

CC vaccine compositions can be modified, for example, to enhance

CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to

CC alter the immune response to suit the target disease. These group-based

CC vaccines allow the focus of an immune response to multiple selected

CC antigens from the same pathogen. Variability among the immune responses

CC of patients can therefore be alleviated by the inclusion of groups from

CC multiple antigens in a vaccine.

SQ Sequence 11 AA:

Query Match 100.0%; Score 41; DB 22; Length 11;
 Best Local Similarity 100.0%; Pred. No. 0.057;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLAKELKFV 9

Db :|||||
 1 vlakelkf 9

RESULT 7

AAU06423 standard; Peptide: 10 AA.
 ID AAU06423

AC AAU06423;

DT 24-OCT-2001 (first entry)

DE Human Leukocyte Antigen-A2 (HLA-A2) supermotif binding peptide #15.

KW Prostate cancer-associated antigen: supermotif; human leukocyte antigen;

KW HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;

KW Immunogenicity; immunosuppression; HTL.

OS Homo sapiens.

PN WO200145728-A2.

PD 28-JUN-2001.

PF 20-DEC-2000; 2000WO-US35516.

PR 21-DEC-1999; 99US-0171312.

PR 07-AUG-2000; 2000US-0633364.

XX (EPIM-) EPIMUNE INC.

XX Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;

PI Keogh E;

PT WPI: 2001-398311/42.

PT Tumour antigen-associated group-based vaccines useful for vaccinating

PT against prostate cancer -

PS Example 2; Page 238; 252pp; English.

CC The sequences represent prostate cancer-associated antigens and derived

CC motif or supermotif epitopes. The peptide epitopes are included in

CC prostate cancer vaccine compositions due to their ability to bind to

CC human leukocyte antigen (HLA) molecules, which recognise the motifs.

CC Peptides with a high binding affinity are further tested for their

CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte

CC (HTL) response. Supermotif-bearing peptides may also be tested for their

CC binding affinity to multiple alleles within the HLA superfamily. The

CC vaccine compositions can be modified, for example, to enhance

CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to

CC alter the immune response to suit the target disease. These group-based

CC vaccines allow the focus of an immune response to multiple selected

CC antigens from the same pathogen. Variability among the immune responses

CC of patients can therefore be alleviated by the inclusion of groups from

CC multiple antigens in a vaccine.

SQ Sequence 10 AA:

Query Match 92.7%; Score 38; DB 22; Length 10;
 Best Local Similarity 88.9%; Pred. No. 0.21;
 Matches 8; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

OY 1 VLAKELKFV 9
 :|||||
 Db 2 llakelkf 10

RESULT 8

AAU06372 standard; Peptide: 9 AA.
 ID AAU06372

XX

AC AAU06372;
 XX 24-OCT-2001 (first entry)
 DE Human Leukocyte Antigen-DR3b (HLA-DR3b) submotif peptide epitope #14.
 XX
 KW Prostate cancer-associated antigen; supermotif; human leukocyte antigen;
 XX HLA; cytotoxic T lymphocyte; helper T lymphocyte; HLA superfamily; CTL;
 KW Immunogenicity; immunosuppression; HTL.
 XX
 OS Homo sapiens.
 XX
 PN MO200145728-A2.
 XX
 PD 28-JUN-2001.
 XX
 PF 20-DEC-2000; 2000MO-US35516.
 XX
 PR 21-DEC-1999; 99US-0171312.
 XX
 PR 07-AUG-2000; 2000US-063364.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Cells E;
 PI Keogh E;
 DR WPI; 2001-398311/42.
 XX
 PT Tumour antigen-associated group-based vaccines useful for vaccinating
 PT against prostate cancer -
 XX
 PS Example 5: Page 235; 252pp; English.
 XX
 CC The sequences represent prostate cancer-associated antigens and derived
 CC motifs or supermotif epitopes. The peptide epitopes are included in
 CC prostate cancer vaccine compositions due to their ability to bind to
 CC human leukocyte antigen (HLA) molecules, which recognise the motifs.
 CC Peptides with a high binding affinity are further tested for their
 CC ability to induce a cytotoxic T lymphocyte (CTL) or a helper T lymphocyte
 CC (HTL) response. Supermotif-bearing peptides may also be tested for their
 CC binding affinity to multiple alleles within the HLA superfamily. The
 CC vaccine compositions can be modified, for example, to enhance
 CC immunogenicity, to avoid the inclusion of immunosuppressive groups, or to
 CC alter the immune response to suit the target disease. These group-based
 CC vaccines allow the focus of an immune response to multiple selected
 CC antigens from the same pathogen. Variability among the immune responses
 CC of patients can therefore be alleviated by the inclusion of groups from
 CC multiple antigens in a vaccine.
 CC
 XX
 SQ Sequence 9 AA:
 Query Match 90.2%; Score 37; DB 22; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 2 LAKELEFV 9
 DB 1 LAKELEFV 8
 RESULT 9
 AAY46778
 ID AAY46778 standard; Peptide; 9 AA.
 AC AAY46778;
 XX
 DT 01-DEC-1999 (first entry)
 XX
 DE Immunogenic peptide having a human leukocyte antigen binding motif #1389.
 XX
 KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;

KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 XX
 OS Synthetic.
 XX
 PN MO9945954-A1.
 XX
 PD 16-SEP-1999.
 XX
 PF 13-MAR-1998; 98MO-US05039.
 XX
 PR 13-MAR-1998; 98MO-US05039.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Kubo RT, Sidney J, Cells E, Grey HW, Southwood S;
 PI WPI; 1999-551214/46.
 DR
 XX
 PT New immunogenic peptides with HLA binding motif, useful in treatment
 PT and diagnosis of cancers and viral diseases -
 XX
 PS Claim 1; Page 84; 150pp; English.
 XX
 CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also
 CC known as human leukocyte antigen (HLA)) binding motif. The immunogenic
 CC peptides can bind to a specific HLA allele (i.e. HLA-A subtypes
 CC HLA-A2.1, A1, A3.2 or A24.1 or HLA-B or C) and induce a cytotoxic T cell
 CC response against the antigen from which the peptide is derived.
 CC Cytotoxic T lymphocytes (CTLs) which destroy antigen-bearing cells are
 CC normally induced by an antigen in the form of a peptide fragment bound
 CC to a HLA molecule, rather than the intact foreign antigen itself, and
 CC are particularly important in tumour rejection and in fighting viral
 CC infections. The peptides are therefore useful therapeutically to treat
 CC or prevent viral infections and cancers in mammals (especially humans)
 CC e.g. prostate cancer, hepatitis B and C, AIDS, and renal carcinoma.
 CC They can be administered as vaccines to elicit an immune response in
 CC individuals susceptible or otherwise at risk of viral infection or
 CC cancer, or used to treat chronic or acute conditions. They are also
 CC useful diagnostically, and can be used to induce a cytotoxic T cell
 CC response, by contacting a cytotoxic T cell with the peptide e.g. to
 CC produce CTLs ex vivo for infusion back into a patient. The
 CC polynucleotides encoding the immunogenic peptides are also useful
 CC therapeutically and for immunisation as above.
 CC
 XX
 SQ Sequence 9 AA:
 Query Match 75.6%; Score 31; DB 20; Length 9;
 Best Local Similarity 100.0%; Pred. No. 6.4e+05;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 OY 1 VLAKELK 7
 DB 3 VLAKELK 9
 RESULT 10
 AAM05203
 ID AAM05203 standard; Peptide; 15 AA.
 AC AAM05203;
 XX
 DT 31-JAN-1997 (first entry)
 XX
 DE Helicobacter Family F (Hsp60) antigen N-terminal peptide.
 XX
 KW Antigen; vaccine; gastroduodenal disease; heat shock protein;
 KW Hsp60.
 XX

XX Protein antigens from *Helicobacter pylori* and their antigenic
 PT fragments - useful for diagnostic detection of specific antibodies
 PT and for vaccination
 PS Example 1; Page 27; 47pp; English.
 CC The present invention describes *Helicobacter pylori* antigens which are
 CC of molecular weight (m.w.) 43-53 kDa, under denaturing and reducing
 CC conditions. The present sequence represents a H. *pylori* antigenic
 CC peptides from an example in the present invention. H. *pylori* antigens
 CC and their fragments are used: (a) for diagnostic detection of H. *pylori*
 CC by detection of specific immunoglobulin G antibodies, particularly in
 CC saliva or blood, and (b) as vaccines for treating or preventing
 CC H. *pylori* infection.
 XX Sequence 8 AA;
 SQ
 Query Match 65.9%; Score 27; DB 19; Length 8;
 Best Local Similarity 83.3%; Pred. No. 6,4e+05;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 3 AKELKF 8
 DB 1 AKELKF 6
 RESULT 13
 ID AAY28976 standard; peptide: 14 AA.
 AC AAY28976;
 XX 04-OCT-1999 (first entry)
 XX Antimicrobial peptide 12.
 XX Antimicrobial: histatin 5; bacterial; fungal; yeast infection;
 KM salivary peptide.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 14
 FT note- "C-terminal amide"
 XX W09937678-A2.
 XX 29-JUL-1999.
 XX 26-JAN-1999; 99WO-NL00045.
 XX 27-JAN-1998; 98NL-1008139.
 XX (TEME-) STICHTING TECH WETENSCHAPPEN.
 XX Helmerhorst EJ, Van Nieuw Amerongen A, Van't Hof W;
 PI Veerman ECI;
 XX WPI: 1999-469115/39.
 DR New antimicrobial peptides with two domains containing mostly
 PT positively charged or unchanged amino acids, e.g. for treating
 PT bacterial or fungal infections
 CC Example 2; Page 9; 28pp; English.
 CC The invention relates to antimicrobial peptides containing a domain of
 CC 10-25 aa in which most aa in one half are positively charged, while most
 CC in the other half are unchanged. These antimicrobial peptides are
 CC synthesised by modifying the C-terminal sequence of histatin 5 peptide.
 CC The peptides are used to treat bacterial, fungal or yeast infections
 CC on the skin, in cattle and in foods. These antimicrobial peptides are
 CC more active than natural salivary peptides (e.g. histatin) and are less
 CC subject to proteolysis and, being rather small, can be produced
 CC relatively inexpensively. They have practically no hemolytic action.
 CC The present sequence represents a specific example of the antimicrobial
 CC peptide of the invention.

CC Typical applications are control of *Candida* and of bacteria in the mouth,
 CC on the skin, in cattle and in foods. These antimicrobial peptides are
 CC more active than natural salivary peptides (e.g. histatin) and are less
 CC subject to proteolysis and, being rather small, can be produced
 CC relatively inexpensively. They have practically no hemolytic action.
 CC The present sequence represents an example of an antimicrobial peptide.
 XX Sequence 14 AA;
 SQ
 Query Match 65.9%; Score 27; DB 20; Length 14;
 Best Local Similarity 85.7%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 LAELKF 8
 DB 3 LAELKF 9
 RESULT 14
 ID AAY28967 standard; peptide: 14 AA.
 AC AAY28967;
 XX 04-OCT-1999 (first entry)
 XX Antimicrobial peptide 3.
 XX Antimicrobial: histatin 5; bacterial; fungal; yeast infection;
 KM salivary peptide.
 OS Synthetic.
 FH Key Location/Qualifiers
 FT Modified-site 14
 FT note- "C-terminal amide"
 XX W09937678-A2.
 XX 29-JUL-1999.
 XX 26-JAN-1999; 99WO-NL00045.
 XX 27-JAN-1998; 98NL-1008139.
 XX (TEME-) STICHTING TECH WETENSCHAPPEN.
 XX Helmerhorst EJ, Van Nieuw Amerongen A, Van't Hof W;
 PI Veerman ECI;
 XX WPI: 1999-469115/39.
 DR New antimicrobial peptides with two domains containing mostly
 PT positively charged or unchanged amino acids, e.g. for treating
 PT bacterial or fungal infections
 CC Claim 8; Page 19; 28pp; English.
 CC The invention relates to antimicrobial peptides containing a domain of
 CC 10-25 aa in which most aa in one half are positively charged, while most
 CC in the other half are unchanged. These antimicrobial peptides are
 CC synthesised by modifying the C-terminal sequence of histatin 5 peptide.
 CC The peptides are used to treat bacterial, fungal or yeast infections
 CC on the skin, in cattle and in foods. These antimicrobial peptides are
 CC more active than natural salivary peptides (e.g. histatin) and are less
 CC subject to proteolysis and, being rather small, can be produced
 CC relatively inexpensively. They have practically no hemolytic action.
 CC The present sequence represents a specific example of the antimicrobial
 CC peptide of the invention.

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LAKELKF 8
| | | | |
Db 3 lfkelft 9

RESULT 15

AAB13937
ID AAB13937 standard; peptide; 14 AA.

AC AAB13937;

DT 16-NOV-2000 (first entry)

DE Type 1 antiviral peptide #3.

KM Antiviral; antiulcer; human immunodeficiency virus; HIV;

KM herpes simplex virus; HSV; cold sore; aphthous ulcer;

XX viral bronchial infection.

CS Synthetic.

XX WC200032629-A2.

PD 08-JUN-2000.

PP 01-DEC-1999; 99MO-NL00732.

XX 01-DEC-1998; 98NL-1010692.

FA (TEME-) STICHTING TECH WETENSCHAPPEN.

PI Van Nieuw Amerongen A, Veerman ECI, Van 't Hof W, Nibbering PH;

XX WPI: 2000-412289/35.

PT Antiviral peptides comprising a domain of 10-25 amino acids, half of

PT which is positively charged and half unchanged, useful for treatment of

PT human immunodeficiency virus and herpes simplex virus -

XX Claim 13: Page 7; 20pp: English.

XX The present invention relates to antiviral peptides containing a domain

XX of 10-25 amino acids, where half the domain is positively charged and

XX the other half is unchanged. The present sequence is a type 1

XX antiviral peptide. Oligomers consisting of at least two peptides

XX coupled together are also included in the invention. The peptides are

XX useful for treating viral infections such as human immunodeficiency

XX virus (HIV) and herpes simplex virus (HSV) and for the treatment of

XX cold sores, aphthous ulcers and viral bronchial infections.

SO Sequence 14 AA:

Query Match 65.9%; Score 27; DB 21; Length 14;

Best Local Similarity 85.7%; Pred. No. 52;

Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LAKELKF 8
| | | | |
Db 3 lfkelft 9

Search completed: August 21, 2002, 15:28:01
Job time: 130 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 21, 2002, 15:26:11 ; Search time 13.02 seconds
(without alignments)
16,884 Million cell updates/sec

Title: US-09-633-364-6827

Perfect score: 41

Sequence: 1 VLAKELKRV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 101902

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Issued_Patents_AA:*
1: /cgn2.6/ptodata/2/1aa/5A.COMB.pep:*
2: /cgn2.6/ptodata/2/1aa/5B.COMB.pep:*
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5: /cgn2.6/ptodata/2/1aa/PCtUS.COMB.pep:*
6: /cgn2.6/ptodata/2/1aa/Backlist1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	28	68.3	8	1	US-08-467-264-19
2	27	65.9	8	2	US-08-467-822-9
3	27	65.9	8	4	US-08-432-697-9
4	27	65.9	8	4	US-08-466-248-9
5	26	63.4	10	1	US-08-284-477-2
6	24	58.5	8	1	US-08-467-264-15
7	24	58.5	12	1	US-08-319-590-11
8	24	58.5	12	1	US-08-487-001A-11
9	24	58.5	12	2	US-08-630-822A-11
10	24	58.5	12	2	US-08-711-905-11
11	24	58.5	12	2	US-08-005-069-11
12	24	58.5	12	2	US-08-465-325-131
13	24	58.5	12	2	US-08-115-737-131
14	24	58.5	12	3	US-08-578-674-10
15	24	58.5	12	4	US-08-311-611A-4
16	24	58.5	12	4	US-08-311-611A-5
17	24	58.5	12	4	US-08-311-611A-5
18	24	58.5	12	4	US-08-311-611A-5
19	24	58.5	12	4	US-08-311-611A-5
20	24	58.5	12	4	US-08-311-611A-5
21	24	58.5	12	4	US-08-311-611A-5
22	24	58.5	12	4	US-08-311-611A-5
23	24	58.5	12	4	US-08-311-611A-5
24	24	58.5	12	4	US-08-311-611A-5
25	24	58.5	12	4	US-08-311-611A-5
26	24	58.5	12	4	US-08-311-611A-5
27	24	58.5	12	4	US-08-311-611A-5

28	22	53.7	15	1	US-08-473-344-5	Sequence 5, Appl1
29	22	53.7	15	2	US-08-621-803-1	Sequence 1, Appl1
30	22	53.7	15	2	US-08-621-803-55	Sequence 55, Appl1
31	22	53.7	15	2	US-08-485-445A-4	Sequence 4, Appl1
32	22	53.7	15	2	US-08-485-445A-5	Sequence 5, Appl1
33	22	53.7	15	3	US-08-414-174-4	Sequence 4, Appl1
34	22	53.7	15	3	US-08-119-263-4	Sequence 4, Appl1
35	22	53.7	15	3	US-08-119-263-5	Sequence 5, Appl1
36	22	53.7	15	4	US-08-657-162-4	Sequence 4, Appl1
37	22	53.7	15	4	US-08-657-162-5	Sequence 5, Appl1
38	22	53.7	15	4	US-09-224-480-4	Sequence 4, Appl1
39	22	53.7	15	4	US-09-224-480-5	Sequence 5, Appl1
40	22	53.7	15	4	US-09-093-539-4	Sequence 4, Appl1
41	22	53.7	15	4	US-09-093-539-5	Sequence 5, Appl1
42	22	53.7	15	4	US-09-217-352-1	Sequence 1, Appl1
43	22	53.7	15	4	US-09-217-352-55	Sequence 55, Appl1
44	22	53.7	15	5	PCt-US94-02465-4	Sequence 4, Appl1
45	22	53.7	15	5	PCt-US94-02465-5	Sequence 5, Appl1

ALIGNMENTS

RESULT 1
US-08-467-264-19
Sequence 19, Application US/08467264
Patent No. 5705156
GENERAL INFORMATION:
APPLICANT: Pastlan, Ira
APPLICANT: FitzGerald, David
TITLE OF INVENTION: Pseudomonas Exotoxins of Low Animal
TITLE OF INVENTION: Cytotoxicity and High Cytocidal Activity
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,264
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/522,182
FILING DATE: 11-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/130,322
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15280-125-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-264-19

Query Match 68.3%, Score 28; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.7e+05;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

OY 1 VLAKELKF 8
DB 1 VISKIKLF 8

RESULT 2
US-08-467-822-9

; Sequence 9, Application US/08467822
; Patent No. 5843460

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Sauerbaum, Sebastien

APPLICANT: Ferrero, Richard L.

APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST

TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE

TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS: 44

ADDRESS: Fimegan, Henderson, Farabow, Garrett &

ADDRESS: Dunne

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,822

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/447,177

FILING DATE: 19-MAY-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/432,697

FILING DATE: 02-MAY-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495, 0137-02000

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STANDARDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-467-822-9

Query Match 65.9%, Score 27; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 AKELKF 8
DB 1 AKELKF 6

RESULT 3
US-08-432-697-9

; Sequence 9, Application US/08432697

; Patent No. 6248330

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Sauerbaum, Sebastien

APPLICANT: Ferrero, Richard L.

APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST

TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE

TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS: 44

ADDRESS: Fimegan, Henderson, Farabow, Garrett &

ADDRESS: Dunne

STREET: 1300 I Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20005-3315

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/432,697

FILING DATE: 02-MAY-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Meyers, Kenneth J.

REGISTRATION NUMBER: 25,146

REFERENCE/DOCKET NUMBER: 03495, 0137-00000

TELEPHONE: (202) 408-4000

TELEFAX: (202) 408-4400

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STANDARDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-432-697-9

Query Match 65.9%, Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 ANELKF 8
DB 1 ANELKF 6

RESULT 4
US-08-466-248-9

; Sequence 9, Application US/08466248

; Patent No. 6258359

GENERAL INFORMATION:

APPLICANT: Labigne, Agnes

APPLICANT: Sauerbaum, Sebastien

APPLICANT: Ferrero, Richard L.

APPLICANT: Thibierge, Jean-Michel

TITLE OF INVENTION: IMMUNOGENIC COMPOSITIONS AGAINST

TITLE OF INVENTION: HELICOBACTER INFECTION, POLYPEPTIDES FOR USE IN THE

TITLE OF INVENTION: COMPOSITIONS, AND NUCLEIC ACID SEQUENCES ENCODING SAID

TITLE OF INVENTION: POLYPEPTIDES

NUMBER OF SEQUENCES: 44

CORRESPONDENCE ADDRESS: 44

```

ADDRESS: Pinegan, Henderson, Farabow, Garrett &
ADDRESSEE: Dunne
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,248
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/447,177
FILING DATE: 19-MAY-1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/432,697
FILING DATE: 02-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Meyers, Kenneth J.
REGISTRATION NUMBER: 25,146
REFERENCE/DOCKET NUMBER: 03495.0137-02000
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-466-248-9

Query Match      65.9%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+05;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Caps 0;

OY      3 AKEIKF 8
Db      1 AKEIKF 6

RESULT 5
US-08-284-477-2
Sequence 2, Application US/08284477
Patent No. 5711881
GENERAL INFORMATION:
APPLICANT: Yanada, Satoko
APPLICANT: Kataoka, Hiroshi
TITLE OF INVENTION: HEMATOPOIETIC INHIBITING FACTOR
TITLE OF INVENTION: CONTAINING COMPOSITIONS
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 601 13th Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

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APPLICATION NUMBER: US/08/284,477
FILING DATE: 06-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Breischneider, Barry E.
REGISTRATION NUMBER: 28,055
REFERENCE/DOCKET NUMBER: 04477/050001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/783-5070
TELEFAX: 202/783-2331
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-284-477-2

Query Match      63.4%; Score 26; DB 1; Length 10;
Best Local Similarity 83.3%; Pred. No. 19;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Caps 0;

OY      3 AKEIKF 8
Db      2 AKEIKF 7

RESULT 6
US-08-467-264-15
Sequence 15, Application US/08467264
Patent No. 5705156
GENERAL INFORMATION:
APPLICANT: Pastan, Ira
APPLICANT: Fitzgerald, David
APPLICANT: Chaudhary, Vijay K.
TITLE OF INVENTION: Pseudomonas Exotoxins of Low Animal
TITLE OF INVENTION: Cytotoxicity and High Cytocidal Activity
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,264
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/522,182
FILING DATE: 11-MAY-1990
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/130,322
FILING DATE: 01-OCT-1993
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 15280-125-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid

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STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-467-264-15

Query Match 58.5%; Score 24; DB 1; Length 8;
Best Local Similarity 50.0%; Pred No. 1.7e+05;
Matches 4; Conservative 4; Mismatches 0; Indels 0;

QY 1 VLAKELF 8
DB 1 VISELEF 8

RESULT 7
US-08-319-590-11
Sequence 11, Application US/08319590
Patent No. 5646115
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: WU HUNTER, SHIRLEY
APPLICANT: WALLENFELS, LYNDIA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND
TITLE OF INVENTION: APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS & MCINTOSH
STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/319,590
FILING DATE: 424
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: VERSER, CAROL TALKINGTON
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-319-590-11

Query Match 58.5%; Score 24; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 5 ELKVF 9
DB 3 ELKVF 7

RESULT 8
US-08-487-001A-11
Sequence 11, Application US/08487001A
Patent No. 5735862
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.

APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDIA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA
TITLE OF INVENTION: PROTEINS AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,001A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-17-C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-487-001A-11

Query Match 58.5%; Score 24; DB 1; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 5 ELKVF 9
DB 3 ELKVF 7

RESULT 9
US-08-630-822A-11
Sequence 11, Application US/08630822A
Patent No. 5840695
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELS, LYNDIA
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,822A
FILING DATE: 11-APR-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-630-822A-11

Query Match 58.5%; Score 24; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ELKRV 9
DB 3 ELKRV 7

RESULT 10
US-08-711-905-11
Sequence 11, Application US/08711905
Patent No. 5927230
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: WU HUNTER, SHIRLEY
APPLICANT: WALLENFELDS, LYNDY
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS AND
TITLE OF INVENTION: APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: SHERIDAN ROSS & MCINTOSH
STREET: 1700 LINCOLN ST., SUITE 3500
CITY: DENVER
STATE: CO
COUNTRY: USA
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/711,905
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: VERSER, CAROL TALKINGTON
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: 2618-17
TELECOMMUNICATION INFORMATION:
TELEPHONE: 303/863-9700
TELEFAX: 303/863-0223
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE:
US-08-711-905-11

Query Match 58.5%; Score 24; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ELKRV 9
DB 3 ELKRV 7

DB 3 ELKRV 7
RESULT 11
US-09-005-069-11
Sequence 11, Application US/09005069
Patent No. 5932470
GENERAL INFORMATION:
APPLICANT: FRANK, GLENN R.
APPLICANT: HUNTER, SHIRLEY WU
APPLICANT: WALLENFELDS, LYNDY
TITLE OF INVENTION: NOVEL ECTOPARASITE SALIVA PROTEINS
TITLE OF INVENTION: AND APPARATUS TO COLLECT SUCH PROTEINS
NUMBER OF SEQUENCES: 107
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/005,069
FILING DATE:
CLASSIFICATION:
Prior Application Data:
APPLICATION NUMBER: 08/630,822
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: CONNELL, GARY J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2618-17-C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-005-069-11

Query Match 58.5%; Score 24; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 ELKRV 9
DB 3 ELKRV 7

RESULT 12
US-08-465-325-131
Sequence 131, Application US/08465325
Patent No. 5686563
GENERAL INFORMATION:
APPLICANT: Magalain Pharmaceuticals Inc.
APPLICANT: 5110 Campus Drive
APPLICANT: Plymouth Meeting, PA 19462
TITLE OF INVENTION: Biologically Active Peptides Having
TITLE OF INVENTION: N-Terminal Substitutions
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finegan, Henderson, Farabow, Garrett &
Dunnet

STREET: 1300 I. Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,325
FILING DATE: 05-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0021-03000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4400
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-465-325-131

Query Match 53.7%; Score 22; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LAKELK 7
1 11111
DB 4 LKELK 9

RESULT 13
US-09-115-737-131
Sequence 131, Application US/09115737
Patent No. 634845
GENERAL INFORMATION:
APPLICANT: U. Prasad Karl
Michael McLane
Taify J. Williams
TITLE OF INVENTION: Biologically Active Peptides with Reduced
Toxicity in Animals and a Method for Preparing Same
NUMBER OF SEQUENCES: 156
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinegan, Henderson, Farabow, Garrett &
Street: 1300 I Street, N.W. Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.3
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,737
FILING DATE: 15-Jul-1998

CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/465,330
FILING DATE: 05-JUN-1995
APPLICATION NUMBER: 08/184,462
FILING DATE: 18-JAN-94
APPLICATION NUMBER: 07/891,201
FILING DATE: 01-JUN-92
ATTORNEY/AGENT INFORMATION:
NAME: Fordis, Jean B
REGISTRATION NUMBER: 32,984
REFERENCE/DOCKET NUMBER: 05387.0021-06000
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 408-4000
TELEFAX: (202) 408-4400
INFORMATION FOR SEQ ID NO: 131:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 131:
US-09-115-737-131

Query Match 53.7%; Score 22; DB 4; Length 11;
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Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 2 LAKELK 7
1 11111
DB 4 LKELK 9

RESULT 14
US-08-578-674-10
Sequence 10, Application US/08578674
Patent No. 6077827
GENERAL INFORMATION:
APPLICANT: Kolbe, Hanno V. J.
APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: KREIL, Gunther
APPLICANT: ACHSTETTER, Tilman
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/578,674
FILING DATE: 28-DEC-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 9400062.9
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meuth, Donna M.

Thu Aug 22 09:00:11 2002

us-09-633-364-6827.rai

Page 7

REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 017753-071
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-12
OTHER INFORMATION: /note="xenoxin-1, alkylated,
US-08-578-674-10
fragment C1(2)"

Query Match 53.7% Score 22; DB 3; Length 12;
Best Local Similarity 71.4% Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 LKTLKF 8
DB 2 LKTLKF 8

RESULT 15
US-09-498-346-10
Sequence 10, Application US/09498346
Patent No. 6277822
GENERAL INFORMATION:
APPLICANT: KOLBE, Hanno V.J.
APPLICANT: RASMUSSEN, Ulla B.
APPLICANT: KREIL, Gunther
APPLICANT: ACHSTER, Tilman
TITLE OF INVENTION: FAMILY OF PEPTIDES KNOWN AS XENOXINS
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS, L.L.P.
STREET: P.O. Box 1404
CITY: Alexandria
STATE: Virginia
COUNTRY: United States
ZIP: 22313-1404
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA/US/09/498,346
FILING DATE: 04 FEB-2000
CLASSIFICATION:
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: US 08/578,674
FILING DATE: 28-DEC-1995
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: FR 90 07901
FILING DATE: 29-JUN-1993
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: FR 94 00202
FILING DATE: 11-JAN-1994
APPLICATION NUMBER: FR 9400062.9
FILING DATE: 11-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Neuth, Donna M.
REGISTRATION NUMBER: 36,607
REFERENCE/DOCKET NUMBER: 017753-071
TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6620
TELEFAX: (703) 836-2021
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1-12
OTHER INFORMATION: /note="xenoxin-1, alkylated,
US-09-498-346-10
fragment C1(2)"

Query Match 53.7% Score 22; DB 4; Length 12;
Best Local Similarity 71.4% Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
OY 2 LKTLKF 8
DB 2 LKTLKF 8

Search completed: August 21, 2002, 15:28:21
Job time: 130 sec


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OY      1 VLAKELKF 8
        1 1 1 1
DB      4 VLCKKORF 11

RESULT 2
ID      MAST_VESMA STANDARD: PRT: 14 AA.
AC      P04205;
DT      20-MAR-1987 (Rel. 04, Created)
DT      20-MAR-1987 (Rel. 04, Last annotation update)
DT      01-AUG-1992 (Rel. 23, Last annotation update)
DE      Mastoparan M (Mast cell-degranulating peptide).
OS      Vespa mandarinia (Hornet).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC      Vespoidea; Vespidae; Vespinae; Vespa.
OX      NCBI_TaxID=7446;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Venom;
RA      Hirai Y., Yasuhara T., Yoshida H., Nakajima T.;
RT      "A new mast cell degranulating peptide, mastoparan-M, in the venom of
RT      the hornet Vespa mandarinia."
RL      Biomed. Res. 24:47-49(1981).
CC      -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC      PIR: A01777; CQVIMM.
DR      Mast cell degranulation; Venom; Amidation.
KW      MOD_RES 14.
FT      MOD_RES 14.
SQ      SEQUENCE 14 AA: 1480 MW: C85ATKCAID7B0DD CRC64;

Query Match 43.9%; Score 18; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 7.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY      2 LAKEKF 6
        1 1 1 1
DB      9 LAKLKF 13

RESULT 3
ID      SYK_CAMUP STANDARD: PRT: 10 AA.
AC      Q46464;
DT      15-DEC-1998 (Rel. 37, Created)
DT      15-DEC-1998 (Rel. 37, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Lysyl-tRNA synthetase (EC 6.1.1.6) (Lysine--tRNA ligase) (LYSRS)
DE      (Fragment).
GN      LYS.
OS      Campylobacter upsaliensis.
OC      Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
OC      Campylobacter.
OX      NCBI_TaxID=28080;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 43954;
RA      MEDLINE=97149302; PubMed=8996110;
RA      Bourke B., Raahid S.T., Bingham H.L., Chan V.L.;
RT      "Characterization of Campylobacter upsaliensis for and its
RT      localization in a highly conserved region of the Campylobacter
RT      genome."
RL      Gene 183:219-224(1996).
CC      -1- CATALYTIC ACTIVITY: ATP + L-lysine + tRNA(Lys) -> AMP + diphosphate
CC      + L-lysyl-tRNA(Lys).
CC      -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC      -1- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration

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CC      between the Swiss Institute of Bioinformatics and the EMBL outstation
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is not commercial
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: L77076; ABA1342.1;
DR      Interpro: IPR002106; AA_TRNA_LIGASE_11.
DR      PROSITE: PS00179; AA_TRNA_LIGASE_11-1; PARTIAL.
DR      PROSITE: PS00339; AA_TRNA_LIGASE_11-2; PARTIAL.
KW      Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
FT      NON_TER 1.
SQ      SEQUENCE 10 AA: 1218 MW: 9C6M46AB1372B05 CRC64;

Query Match 41.5%; Score 17; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 8.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

OY      2 LAKEKF 7
        1 1 1 1
DB      1 LKSEKF 6

RESULT 4
ID      CH60_CANFA STANDARD: PRT: 13 AA.
AC      P49818;
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      60 kDa heat shock protein, mitochondrial (Hsp60) (60 kDa chaperonin)
DE      (Cpn60) (heat shock protein 60) (Hsp-60) (Mitochondrial matrix protein
DE      P1) (Fragment).
DR      HSP60 OR HSP60.
GN      Canis familiaris (Dog).
OS      Canis familiaris (Dog).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX      NCBI_TaxID=9615;
RN      [1]
RP      SEQUENCE.
RC      TISSUE=Heart;
RA      MEDLINE=98163340; PubMed=9504812;
RA      Dunn M.J., Corbett J.M., Wheeler C.H.;
RT      "HSC-2DPAGE and the two-dimensional gel electrophoresis database of
RT      dot heart proteins."
RL      Electrophoresis 18:2795-2802(1997).
CC      -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND
CC      MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF
CC      IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE
CC      REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED
CC      UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX.
CC      -1- SUBCELLULAR LOCATION: Mitochondrial matrix.
CC      -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
DR      HSC-2DPAGE: P49818; DOG.
DR      Interpro: IPR001844; Chaperonins_cpn60.
DR      PROSITE: PS00296; CHAPERONINS_CPN60; PARTIAL.
KW      Chaperone; ATP-binding; Mitochondrion.
FT      NON_TER 13.
SQ      SEQUENCE 13 AA: 1383 MW: C657IE012DBFE879 CRC64;

Query Match 41.5%; Score 17; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0.

OY      3 AKELKF 8
        1 1 1 1
DB      1 AKDYKF 6

RESULT 5

```

[illegible]

OY 1 VLAKELK 7
 Db 2 VILKAIR 8
 RESULT 7
 ID MAST_VESLE STANDARD: PRT: 14 AA.
 AC P01514;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE Mastoparan.
 DE Vesputia lewisii (yellow jacket) (Vesp.).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Melopota; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Vespoidae; Vespidae; Vespinae; Vespula.
 OC NCBI_TaxID=432;
 RN 11
 RE SEQUENCE AND SYNTHESIS.
 RE TISSUE=Venom.
 RX MEDLINE=80155337; PubMed=540352;
 RX Hirai Y., Yasuhara T., Yoshida H., Nakajima T., Fujino M., Kitada C.;
 PT "A new mast cell degranulating peptide 'mastoparan' in the venom of
 Vesputia lewisii.";
 CC Chem. Pharm. Bull. 27:1942-1944 (1979).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
 THAT COUPLE TO PHOSPHOLIPASE C.
 DR PIR: A01776; OMAVV.
 DR Mast cell degranulation; Venom; Amidation.
 FT MOD_RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA: 1480 MM: CC0C0CEAD1D7800DD CRC64:
 QY 2 LAKEL 6 39.0%; Score 16; DB 1; Length 14;
 Db 9 LAKKI 13 Best Local Similarity 60.0%; Pred. No. 1.9e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 0;
 RESULT 8
 ID MAST_VESXA STANDARD: PRT: 14 AA.
 AC P01515;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1994 (Rel. 38, Last annotation update)
 DE Mastoparan X (MP-X).
 DE Vesputia lewisii (Japanese hornet).
 OS Euparagordata; Neoptera; Tracheata; Tracheata; Hexapoda; Insecta;
 OS Pterygota; Melopota; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Vespoidae; Vespidae; Vespinae; Vespa.
 OC NCBI_TaxID=7448;
 RN 11
 RE SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=80155338; PubMed=540363;
 RA Hirai Y., Kuwada M., Yasuhara T., Yoshida H., Nakajima T.;
 RT "A new mast cell degranulating peptide homologous to mastoparan in
 the venom of Japanese hornet (Vespa xanthoptera).";
 RL Chem. Pharm. Bull. 27:1945-1946 (1979).
 RN 12
 RP STRUCTURE BY NMR.
 RX MEDLINE=92304942; PubMed=1610813;
 RA Wakamatsu K., Okada A., Miyazawa T., Ohya M., Higashijima T.;
 RT "Membrane-bound conformation of mastoparan X, a G-protein-activating
 peptide.";
 RL Biochemistry 31:5654-5660 (1992).
 RN 13

STRUCTURE BY NMR. PubMed-9537994;
 MEDLINE-98206894; PubMed-9537994;
 Kusunoki H., Makamatsu K., Sato K., Miyazawa T., Kohno T.;
 "G protein-bound conformation of mastoparan-X: heteronuclear
 multiple resonance transferred nuclear Overhauser effect analysis of
 peptide uniformly enriched with ¹³C and ¹⁵N";
 Biochemistry 37:4782-4790(1998)
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
 CC THAT COUPLE TO PHOSPHOLIPASE C.
 DR PIR: A01778; QNWXKX.
 DR PDB: 1A13; 16-FEB-99.
 CC MAST CELL DEGRANULATION: Venom. Amidation: 3D-structure.
 CC MOD.RES 14
 CC AMIDATION: 14
 CC MOD.RES 14
 CC SEQUENCE 14 AA: 1557 MW: C85DE0D7AA7AB0DD CRC64:

Query Match 39.0%; Score 16; DB 1; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.9e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 LAKEL 6
 DB 9 MAKKL 13

RESULT 9
 ID ACBA.ACICA STANDARD; PRT: 15 AA.
 AC P28467;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 D3 Isocitrate lyase (EC 4.1.3.1) (isocitrate) (ICL)
 D3 (Fragment).
 G4 ACBA.
 CC Acinetobacter calcoaceticus.
 CC Bacteria: Proteobacteria; gamma subdivision; Moraxellaceae;
 CC Acinetobacter.
 CC NCBI_TaxID-471;
 CC [1]
 CC SEQUENCE:
 CC MEDLINE-92041568; PubMed-1938889;
 CC Hoyt J.C., Johnson K.E., Reeves H.C.;
 CC "Purification and characterization of Acinetobacter calcoaceticus
 CC isocitrate lyase";
 CC J. Bacteriol. 173:6844-6848(1991).
 CC -1- CATALYTIC ACTIVITY: isocitrate - succinate + glyoxylate.
 CC -1- PATHWAY: FIRST STEP IN GLYOXYLATE BYPASS, AN ALTERNATIVE TO THE
 CC TRICARBOXYLIC ACID CYCLE (IN BACTERIA, PLANTS, AND FUNGI).
 CC -1- SUBUNIT: HOMOTETRAMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC PIR: A4138; A4138.
 CC InterPro: IPR000918; Isocit_Lyase.
 CC PROSITE: PS00161; ISOCITRATE LYASE; PARTIAL.
 CC Glyoxylate bypass; Tricarboxylic acid cycle; Lyase.
 CC NON TER 15
 CC SEQUENCE 15 AA: 1710 MW: 83AE726B1F2F96B3 CRC64:

Query Match 39.0%; Score 16; DB 1; Length 15;
 Best Local Similarity 75.0%; Pred. No. 2e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 KELK 7
 DB 11 RELK 14

RESULT 10
 ID CRBL.VESXA STANDARD; PRT: 13 AA.
 AC P17234;

DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Vespid Chemotactic Peptide X (VESP-X).
 OS Vespa xanthoptera (Japanese hornet).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Pleurogata; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 CC Vespoidea; Vespidae; Vespinae; Vespa.
 CC NCBI_TaxID-7446;
 CC [1]
 CC SEQUENCE:
 CC TISSUE-Venom:
 CC Yasuhara T., Ito Kawa H., Suzuki N., Nakamura H., Nakajima T.;
 CC (in) Izumiya N. (eds.);
 CC Peptide Chemistry 1984, pp.177-182, Protein Research Foundation,
 CC Osaka (1985).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
 CC OF NEUTROPHILS.
 CC MAST CELL DEGRANULATION: Chemotaxis: Venom. Amidation.
 CC MOD.RES 13
 CC AMIDATION: 13
 CC SEQUENCE 13 AA: 1368 MW: C85040365D9233D CRC64:

Query Match 36.6%; Score 15; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2.9e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 VLAKEL 6
 DB 4 IIAKLL 9

RESULT 11
 ID CRBL.VESOR STANDARD; PRT: 14 AA.
 AC P17236;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last annotation update)
 DE Histamine releasing peptide II (HR-II).
 DE Vespa orientalis (oriental hornet).
 CC Eukaryota; Metazoa; Arthropoda; Tracheata; Insecta;
 CC Pleurogata; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 CC Vespoidea; Vespidae; Vespinae; Vespa.
 CC NCBI_TaxID-7447;
 CC [1]
 CC SEQUENCE:
 CC TISSUE-Venom:
 CC Miroshnikov A.I., Saezhkova L.G., Nazimov I.V., Reshetova O.I.,
 CC Rozyanov B.V., Gushchin I.S.;
 CC "Structure and properties of histamine releasing peptides from the
 CC venom of Vespa orientalis hornet";
 CC Bioorg. Khim. 7:1467-1477(1981).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
 CC OF NEUTROPHILS.
 CC MAST CELL DEGRANULATION: Chemotaxis: Venom. Amidation.
 CC MOD.RES 14
 CC AMIDATION: 14
 CC SEQUENCE 14 AA: 1524 MW: 22015B4A6CEDFD38 CRC64:

Query Match 36.6%; Score 15; DB 1; Length 14;
 Best Local Similarity 42.9%; Pred. No. 3.1e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 VLAKEL 7
 DB 5 ILGKLV 11

RESULT 12
 ID COXI.THUOB STANDARD; PRT: 15 AA.
 COXI THUOB

CC	01-NOV-1997 (Rel. 35, Created)
CC	01-NOV-1997 (Rel. 35, Last sequence update)
CC	01-NOV-1997 (Rel. 35, Last annotation update)
CC	Cytochrome c oxidase polypeptide VIC-2 (EC 1.9.3.1) (Fragments).
CC	Thunnus obsesus (Bigeye tuna).
CC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC	Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
CC	Acantloporhina; Acanthopterygii; Percormorpha; Perciliformes; Scombroidei;
CC	Scombridae; Thunnus.
CC	NCBI_TaxId=8241;
CC	11
CC	SEQUENCE.
CC	TISSUE=Heart;
CC	MEDLINE=97454291; PubMed=9310366;
CC	Arnold S., Lee I., Kim M., Song E., Linder D., Lottspeich F.,
CC	Kadenbach B.;
CC	"The subunit structure of cytochrome-c oxidase from tuna heart and
CC	liver."
CC	Eur. J. Biochem. 248:99-103(1997).
CC	-1- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE
CC	CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN
CC	MITOCHONDRIAL ELECTRON TRANSPORT.
CC	-1- CATALYTIC ACTIVITY: 4 ferriocytochrome c + O(2) -> 4 ferriocytochromes
CC	c + 2 H(2)O.
CC	-1- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC	Oxidoreductase; Inner membrane; Mitochondrion.
CC	NON_TER 1
CC	NON_CONS 8
CC	FT 9
CC	NON_TER 15
CC	FT 15
CC	SEQUENCE 15 AA: 1696 MW: 464C966C73A40294 CRC64;

```

Query Match Score 15: DB 1: Length 15:
Best Local Similarity 60.08;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 1 VLAKE 5
1:11
db 5 VYAKK 9

```

RESULT	13			
ID	R13A_SPTOL	STANDARD:	PRT:	15 AA.
AC	P82454;			
DT	01-MAR-2002 (Rel. 41, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	60S ribosomal protein L13a (Fragment).			
GN	RP13A.			
OS	Spinacia oleracea (Spinach).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;			
OC	Caryophyllales; Caryophyllales; Chenopodiaceae; Spinacia.			
NCBI	Taxid:3562;			
RN	[1]			
RP	SEQUENCE.			
RC	STRAIN-CV, ALVARO; TISSUE-Leaf;			
RA	Yamauchi K., Subramanian A.R.;			
RT	"N-terminal sequence of spinach cytosolic 60S ribosomal protein			
RT	L13a."			
RL	Submitted (Apr-2000) to the SWISS-PROT data bank.			
RC	-1- SIMILARITY: BELONGS TO THE SM13-PROT FAMILY OF RIBOSOMAL			
DR	Interpro: IPRO01074: RIBOSOMAL_L13.			
DR	Prosite: PS00783: RIBOSOMA_L13; PARTIAL.			
FT	KW RIBOSOMAL PROTEIN.			
FT	NON_TER 15			
SD	SEQUENCE 15 AA; 1409 MW; C7B9C0F5A099EB3 CRC64;			
Query Match	36.6%;	Score 15;	DB 1;	Length 15;
Best Local Similarity	33.3%;	Pred. NO. 3.4e+03;		

Matches	2;	Conservative	3;	Mismatches	1;	Indels	0;	Gaps	0;
Qy	1	VLAKEL	6	:	1	1	1	:	
Db	6	IMAKRY	11	:					

RESULT	14
ID	COXO_SHEEP
AC	P80337;
DT	01-OCT-1994 (Rel. 30, Created)
DT	01-OCT-1994 (Rel. 30, Last sequence update)
DT	01-OCT-1994 (Rel. 30, Last annotation update)
DE	Cytochrome c oxidase polypeptide VII α -liver/heart (Ec 1.9.3.1) (Fragment).
OS	Ovis aries (Sheep).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC	Bovidae; Caprinae; Ovis.
OX	NCBI_TaxID=9940;
RN	[1]
RP	SEQUENCE.
RC	TISSUE=heart, and liver;
RA	Preuss R., Kadenbach B.;
RL	Submitted (MAR-1994) to the SWISS-PROT data bank.
CC	-!- FUNCTION: THIS PROTEIN IS ONE OF THE NUCLEAR-CODED POLYPEPTIDE CHAINS OF CYTOCHROME C OXIDASE, THE TERMINAL OXIDASE IN MITOCHONDRIAL ELECTRON TRANSPORT.
CC	-!- CATALYTIC ACTIVITY: 4 ferrocyclochrome c + O(2) = 4 ferriycytochrome c + 2 H(2)O.
CC	oxidoreductase; Mitochondion.
KW	NON_TER
FT	10
SO	SEQUENCE 10 AA: 1027 MW: cAE95CA33DC7633D CMC64;

Query Match	34.18;	Score 14;	DB 1;	Length 10;
Best Local Similarity	42.98;	Pred. No. 3.7e+03;		
Matches	3;	Conservative	3;	Indels 0; Gaps 0.

RESULT	15			
ID	RL16	ACHLA	STANDARD:	PRT: 10 AA.
AC	P299221			
DT	01-DEC-1992 (rel. 24, Created)			
DT	01-DEC-1992 (rel. 24, Last sequence update)			
DT	01-NOV-1995 (rel. 32, Last annotation update)			
DE	50S ribosomal protein L16 (Fragment).			
GN	RLP.			
GN	Acholeplasma laidlawii.			
OC	Bacteria: Firmicutes: Bacillus/Clostridium group: Mollicutes;			
OC	Acholeplasmataceae: Acholeplasma.			
OX	NCBI_TaxID=2148;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=92210505; Pubmed=1556079;			
RA	Lam P.O., Sears B.B.;			
RT	Evolutionary relationships of a plant-pathogenic mycoplasma like			
RT	organism and Acholeplasma laidlawii deduced from two ribosomal protein			
RT	gene sequences.";			
RL	J. Bacteriol. 174:2606-2611(1992).			
CC	-1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS			
CC	LOCATED AT THE A SITE OF THE PEPTIDYLTRANSFERASE CENTER			
CC	(BY SIMILARITY).			
CC	-1- SIMILARITY: BELONGS TO THE L16P FAMILY OF RIBOSOMAL PROTEINS.			
CC	THIS SWISS-PROT entry is copyright. It is produced through a collaboration			
CC	between The Swiss Institute of Bioinformatics and the EMBL outstation			

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CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC EMBL; M74771; AAA21914.1; .
DR PIR; F41839; F41839.
DR InterPro; IPR000114; RIBOSOMAL_L16.
DR PROSITE; PS00586; RIBOSOMAL_L16_1; PARTIAL.
DR PROSITE; PS00701; RIBOSOMAL_L16_2; PARTIAL.
KW Ribosomal protein; rRNA-binding.
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 1324 MW; B3366A21B4032766 CRC64;

Query Match 34.1%; Score 14; DB 1; Length 10;
Best Local Similarity 25.0%; Pred. No. 3.7e+03;
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

OY 1 VLAKELKF 8
Db 2 LMPKRTKY 9

Search completed: August 21, 2002, 15:31:51
Job time: 204 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: August 21, 2002, 15:27:11 ; Search time 14.12 seconds
(without alignments)
61.247 Million cell updates/sec

Title: US-09-633-364-6827
Perfect score: 41
Sequence: 1 VLAKELFV 9

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 28338 seqs, 9608934 residues

Total number of hits satisfying chosen parameters: 2519

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: PIR_71:*

1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	58.5	11	2	PC2372
2	20	48.8	15	2	B4136
3	19	46.3	10	2	A44871
4	19	46.3	14	2	S72217
5	18	43.9	13	2	S28425
6	18	43.9	14	1	OMVHMM
7	18	43.9	14	2	PC2373
8	17	41.5	14	2	PN0147
9	17	41.5	15	2	PA0053
10	16.5	40.2	12	2	S01322
11	16	39.0	10	2	PS0254
12	16	39.0	10	2	S48182
13	16	39.0	12	2	C36201
14	16	39.0	12	2	S47360
15	16	39.0	14	1	OMVHMM
16	16	39.0	14	1	OMVHMM
17	16	39.0	14	1	OMVHMM
18	16	39.0	14	2	PN0151
19	16	39.0	15	2	PN0117
20	16	39.0	15	2	A41338
21	16	39.0	15	2	S36890
22	15	36.6	10	2	S06964
23	15	36.6	10	2	S38304
24	15	36.6	11	2	S33519
25	15	36.6	12	2	A58501
26	15	36.6	13	2	A61288
27	15	36.6	14	2	JM0390
28	15	36.6	14	2	S29789
29	15	36.6	15	2	PA0097

30	15	36.6	15	2	I50503
31	15	36.6	15	2	S77987
32	14	34.1	9	2	G58502
33	14	34.1	9	2	I54379
34	14	34.1	9	2	B30572
35	14	34.1	10	2	F41839
36	14	34.1	10	2	PH0113
37	14	34.1	10	2	C10572
38	14	34.1	11	2	S56606
39	14	34.1	11	2	B39853
40	14	34.1	11	2	C59151
41	14	34.1	11	2	H84082
42	14	34.1	12	2	S15835
43	14	34.1	12	2	G48215
44	14	34.1	12	2	S69402
45	14	34.1	12	2	PH1466

ALIGNMENTS

RESULT 1
PC2372
58K heat shock protein:groEL [similarity] - Bacillus cereus (strain ts-4) (fragment)
C:Species: Bacillus cereus
C>Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: PC2372
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatano, S
Biosci. Biotechnol. Biochem. 59, 231-235, 1995
A:Title: Identification of DNA-binding proteins changed after induction of sporula
A:Reference number: PC2369; MUID:95218265
A:Accession: PC2372
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <MS>
C:Keywords: heat shock; molecular chaperone; stress-induced protein

Query Match
Best Local Similarity 58.5% Score 24; DB 2; Length 11;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
B4136
ovostatin - green sea turtle (fragment)
C:Species: Chelonia mydas (green sea turtle)
C>Date: 21-Apr-1992 #sequence_revision 21-Apr-1992 #text_change 18-Jun-1993
C:Accession: B4136
R:Osada, T.; Sasaki, T.; Ikat, A.
J. Biochem. 103, 212-217, 1988
A:Title: Purification and characterization of alpha-macroglobulin and ovomacroglobulin
A:Reference number: A41436; MUID:88227890
A:Accession: B41436
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OS>

Query Match
Best Local Similarity 48.8% Score 20; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AKELFV 9
DB 2 APELOLV 8
RESULT 3

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M44871
monodehydroascorbate reductase (NADH) (EC 1.6.5.4) - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 12-Sep-1997
C:Accession: M44871
R:Dalton, D.A.; Langeberg, L.; Robbins, M.
R:Biochem. Biophys. 297, 281-286, 1992
A:Title: Purification and characterization of monodehydroascorbate reductase from soybean
A:Reference number: M44871; MUID:92088257
A:Accession: M44871
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-10 <DAL>
A:Experimental source: root nodules, cv. Williams
A:Note: sequence extracted from NCBI backbone (NCBIP:71052)
C:Keywords: oxidoreductase

Query Match          46.3%; Score 19; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 7.3e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 AKELFV 9
    1 1 1 1
    1 AKELFV 7
DB 1 AKELFV 7

RESULT 4
S72217
D:arabinose 1-dehydrogenase (NAD(P)+) (EC 1.1.1.117) - yeast (Candida albicans) (fragment)
C:Species: Candida albicans
C:Date: 29-Jan-1998 #sequence_revision 06-Feb-1998 #text_change 13-Mar-1998
C:Accession: S72217
R:Kim, S.T.; Huh, W.K.; Kim, J.Y.; Hwang, S.W.; Kang, S.O.
R:Biochim. Biophys. Acta 1297, 1-8, 1996
A:Title: D-arabinose dehydrogenase and biosynthesis of erythroascorbic acid in Candida
A:Reference number: S72217; MUID:96439039
A:Accession: S72217
A:Molecule type: protein
A:Residues: 1-14 <KIM>
C:Keywords: oxidoreductase

Query Match          46.3%; Score 19; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 2 LAELKF 8
    1 1 1 1
    1 LAELKF 9
DB 3 LAELKF 9

RESULT 5
S28423
D:protein - rape (fragment)
C:Species: Brassica napus (rape)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 13-Jan-1995
C:Accession: S28423
R:Wells, A.; Leadley, P.F.; Slabas, A.R.
R:Plant Mol. Biol. 20, 763-780, 1992
A:Title: Induction, purification and characterisation of acyl-ACP thioesterase from develope
A:Reference number: S28424; MUID:93099229
A:Accession: S28425
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-13 <WEL>

Query Match          43.9%; Score 18; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLAKEL 6

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DB 7 ITAKEL 12
    1 1 1 1
    1 ITAKEL 12

RESULT 6
OMVHM
Mastoparan M - hornet (Vespa mandarinia)
N:Alternate names: mast cell degranulating peptide
C:Species: Vespa mandarinia
C:Date: 04-Dec-1986 #sequence_revision 04-Dec-1986 #text_change 08-Dec-1995
C:Accession: A01777
R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
R:Blomet. Res. 2, 447-449, 1981
A:Title: A new mast cell degranulating peptide, mastoparan-M, in the venom of the
A:Reference number: A01777
A:Accession: A01777
A:Molecule type: protein
A:Residues: 1-14 <HIR>
C:Comment: This cytoactive peptide from hornet venom induces mast cell degranulation
C:Superfamily: mastoparan
C:Keywords: amidated carboxyl end; venom
F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match          43.9%; Score 18; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAEL 6
    1 1 1 1
    1 LAEL 13
DB 9 LAEL 13

RESULT 7
PC2373
D:probable IMP dehydrogenase (EC 1.1.1.205) [similarity] - Bacillus cereus (strain ts
C:Species: Bacillus cereus
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
C:Accession: PC2373
R:Matsumoto, K.; Miyamoto, T.; Yamaguchi, K.; Sayed, M.A.; Kajiwara, T.; Hatanaka, S.
R:Biochem. Biophys. Res. Commun. 231, 231-235, 1997
A:Title: Identification of DNA-binding proteins changed after induction of sporulation
A:Reference number: PC2369; MUID:95218265
A:Accession: PC2373
A:Status: Preliminary
A:Molecule type: protein
A:Residues: 1-14 <MAS>
C:Superfamily: IMP dehydrogenase; CBS homology; IMP dehydrogenase amino-terminal h
C:Keywords: GMP biosynthesis; NAD; oxidoreductase; purine nucleotide biosynthesis

Query Match          43.9%; Score 18; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 ELKLV 9
    1 1 1 1
    1 ELKLV 7
DB 3 ELKLV 7

RESULT 8
PN0147
D:omega-glucanase 1 and 2 - Aegilops longissima (fragment)
C:Species: Aegilops longissima
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: PN0147; PN0146
R:Odintsova, T.I.; Egorov, T.A.
R:Biokhimiya 55, 509-516, 1990
A:Title: N-terminal sequences of omega-glucanases of Aegilops longissima: On the ori
A:Reference number: PN0147; MUID:90283493
A:Accession: PN0147
A:Molecule type: protein
A:Residues: 1-14 <ODI>

```

A: Experimental source: strain K-202
A: Note: omega-glutidine 2 (amino-terminal fragment)
A: Accession: P01046
A: Molecule type: Protein
A: Residues: 1-9 <CD2>
A: Experimental source: strain K-202
A: Note: omega-glutidine 1 (amino-terminal fragment)

Query Match 41.5%; Score 17; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 LAKEIK 7
DB 7 IGKEIK 12

RESULT 9
PA0053
protein QP200006 - fungus (Fusarium sporotrichioides) (fragment)
C: Species: Fusarium sporotrichioides
C: Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C: Accession: PA0053
R: Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
Submitted to JIPID, October 1994
A: Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A: Reference number: PA0051
A: Accession: PA0053
A: Molecule type: Protein
A: Residues: 1-15 <CHO>

Query Match 41.5%; Score 17; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 AKELKPV 9
DB 2 AKELKPI 8

RESULT 10
S01222
translation elongation factor EF-Tu - Pseudomonas aeruginosa (fragment)
C: Species: Pseudomonas aeruginosa
C: Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 26-Aug-1999
C: Accession: S01222
R: Hughes, M.A.; Jones, D.S.
Nucleic Acids Res. 16, 7193, 1988
A: Title: A fragment of the Pseudomonas aeruginosa genome contains five rRNA genes, four
A: Reference number: S01222; M01D:8303352
A: Accession: S01222
A: Status: translation not shown
A: Molecule type: DNA
A: Residues: 1-12 <RHG>
A: Cross-References: EMBL:X07950; NID:945426; PIDN:CAA30775.1; PID:945427
C: Genetics:
A: Gene: tuftB
C: Superfamily: translation elongation factor Tu; translation elongation factor Tu homolog
C: Keywords: GTP binding; protein biosynthesis

Query Match 40.2%; Score 16.5; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 3e+03; 0; Indels 1; Gaps 1;
Matches 5; Conservative 1; Mismatches 0;

OY 2 LAKEIKF 8
DB 1 MAKE-KF 6

RESULT 11

PS0254
18k protein 5507 - rice (strain Nihonbare) (fragment)
C: Species: Oryza sativa (rice)
C: Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C: Accession: PS0254
R: Acetia, A.
Submitted to JIPID, April 1993
A: Reference number: PS0206
A: Accession: PS0254
A: Molecule type: Protein
A: Residues: 1-7 <TSU>
A: Experimental source: leaf, chloroplast, strain Nihonbare
A: Note: molecular weight 18k, pI 4.4

Query Match 39.0%; Score 16; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKE 5
DB 3 LAKE 6

RESULT 12
S48182
bacterioferritin - Rhodobacter capsulatus
C: Species: Rhodobacter capsulatus
C: Date: 15-Jul-1995 #sequence_revision 19-Oct-1995 #text_change 07-May-1999
C: Accession: S48182
R: Ringeling, P.L.; Davy, S.L.; Monkara, F.A.; Hunt, C.; Dickson, D.P.E.; McEwan, J.
Eur. J. Biochem. 223, 847-855, 1994
A: Title: Iron metabolism in Rhodobacter capsulatus. Characterisation of bacterioferritin
A: Reference number: S48182; M01D:94333089
A: Accession: S48182
A: Status: preliminary
A: Molecule type: Protein
A: Residues: 1-10 <KIM>

Query Match 39.0%; Score 16; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 3 AKELK 8
DB 5 AKYIEF 10

RESULT 13
C36201
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment)
C: Species: Malus domestica (apple tree)
C: Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 04-Feb-2000
C: Accession: C36201; C33103
R: YIP, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990
A: Title: Characterization and sequencing of the active site of 1-aminocyclopropane
A: Reference number: A36201; M01D:91045911
A: Accession: C36201
A: Molecule type: Protein
A: Residues: 1-12 <YIP>
A: Experimental source: strain Golden delicious
C: Superfamily: 1-aminocyclopropane-1-carboxylate synthase
C: Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal
F4/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 39.0%; Score 16; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKE 6


```

ESL_LACCA
ID ESL_LACCA STANDARD: PRT: 10 AA.
AC P81758:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Putative esterase/lipase (EC 3.1.-.-) (Fragment).
OS Lactobacillus casei.
OC Bacteriia; Firmicutes; Bacillus/Clostridium group; Lactobacillaceae;
OC Lactobacillus.
OX NCBI_TaxID=1582;
RN [1]
RP SEQUENCE.
RC STRAIN=TEP731;
RA Lopez de Felipe F.;
RL Submitted (MAR-1999) to the SWISS-PROT data bank.
KM Hydrolyase; Serine esterase.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1070 MW: 106132D732CAB1A0 CRC64;

Query Match 39.0%; Score 16; DB 1; Length 10;
Best Local Similarity 80.0%; Pred. No. 1.de+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLAKEL 5
DB 6 VLAKEL 10

RESULT 6
RS19_ASHYP STANDARD: PRT: 13 AA.
ID RS19_ASHYP
AC 044592:
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 30S Ribosomal protein S19 (Fragment).
CN RRS OR RPS19.
OS Ash yellow's phytoplasm.
OC Bacteriia; Firmicutes; Bacillus/Clostridium group; Mollicutes;
OC Achaetoplasmataceae; Phytoplasmata.
OX NCBI_TaxID=35780;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94350802; PubMed=8071198;
RA Gundersen D.E., Lee I.M., Rehner S.A., Davis R.E., Kingsbury D.T.;
RT "Phylogeny of mycoplasma-like organisms (phytoplasmata): a basis for
RT their classification."
RL J. Bacteriol. 176:5244-5254(1994).
CC -1- FUNCTION: PROTEIN S19 FORMS A COMPLEX WITH S13 THAT BINDS STRONGLY
CC TO THE 16S RIBOSOMAL RNA (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE S19P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation-
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CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L26699; AA883936.1;
DR InterPro: IPR002222; RIBOSOMAL_S19;
DR PROSITE: PS00133; RIBOSOMAL_S19; PARTIAL.
KM Ribosomal protein; rRNA-binding.
FT NON_TER 1
SQ SEQUENCE 13 AA: 1433 MW: C8CA010B84E5305D CRC64;

Thu Aug 22 09:00:13 2002
Score 16; DB 1; Length 13;
Pred. No. 1.de+03;
Indels 0; Gaps 0;

OY 1 VLAKEL 7
DB 2 VLAKEL 8

RESULT 7
MAST_VESLE STANDARD: PRT: 14 AA.
ID MAST_VESLE
AC P01514:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Mastoparan.
OS Vesputa lewisii (Yellow jacket) (Vesp).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vesputidae; Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7452;
RN [1]
RP SEQUENCE, AND SYNTHESIS.
RC TISSUE=Venom;
RA MEDLINE=80155337; PubMed=540362;
RA Hirai Y., Yasuhara T., Yoshida H., Nakajima T., Fujino M., Kitada C.;
RT "A new mast cell degranulating peptide 'mastoparan' in the venom of
RT Vesputa lewisii."
RL Chem. Pharm. Bull. 27:1942-1944(1979).
CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. ACTIVATES G PROTEINS
CC THAT COUPLE TO PHOSPHOLIPASE C.
DR PIR: A01776; OMWAVV.
KM Mast cell degranulation; Venom; Amidation.
FT MOD_RES 14
SQ SEQUENCE 14 AA: 1480 MW: CC0CECA1D7B00DD CRC64;

Query Match 39.0%; Score 16; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.9e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKEL 6
DB 9 LAKEL 13

RESULT 8
MAST_VESXA STANDARD: PRT: 14 AA.
ID MAST_VESXA
AC P01515:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Mastoparan X (MP-X).
OS Vespa xanthoptera (Japanese hornet).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
OC Vesputidae; Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7448;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA MEDLINE=80155338; PubMed=540363;
RA Hirai Y., Kuwada M., Yasuhara T., Yoshida H., Nakajima T.;
RT "A new mast cell degranulating peptide homologous to mastoparan in
RT the venom of Japanese hornet (Vespa xanthoptera)."
RL Chem. Pharm. Bull. 27:1945-1946(1979).
RN [2]
RP STRUCTURE BY NMR.
RA MEDLINE=92304942; PubMed=1610813;
RA Wakematsu K., Okada A., Miyazawa T., Ohya M., Higashijima T.;
RT "Membrane-bound conformation of mastoparan X, a G-protein-activating
RT peptide."
RL Biochemistry 31:5654-5660(1992).
RN [3]

```

Db 2 LSKOL 6

RESULT 14

S47360
T-cell antigen receptor VJ junction beta chain - human
C:Species: Homo sapiens (man)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1995
C:Accession: S47360
R:Lehner, P. J.
submitted to the EMBL Data Library, August 1994
A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T
A:Reference number: S47355
A:Accession: S47360
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-12 <LEH>
A:Cross-references: EMBL:Z35684; NID:9527457; PID:CA84753.1; PID:9527458
C:Keywords: T-cell receptor

Query Match

39.0%; Score 16; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 AKEL 6

Db 6 AKEL 9

RESULT 15

OMNAV

mastoparan - yellowjacket (Vespula lewisii)
C:Species: Vespula lewisii
C:Date: 24-Sep-1981 #sequence_revision 24-Sep-1981 #text_change 08-Dec-1995
C:Accession: A01776
R:Hirai, Y.; Yasuhara, T.; Yoshida, H.; Nakajima, T.; Fujino, M.; Kitada, C.
Chem. Pharm. Bull. 27, 1942-1944, 1979
A:title: A new mast cell degranulating peptide mastoparan in the venom of Vespula-lewisii
A:Reference number: A01776; MUID:80155337
A:Accession: A01776
A:Molecule type: protein
A:Residues: 1-14 <HIR>
A:Note: the active peptide was also synthesized
C:Comment: This cytotoxic peptide from wasp venom induces mast cell degranulation. The
C:Superfamily: mastoparan
C:Keywords: amidated carboxyl end
F:14/Modified site: amidated carboxyl end (Leu) #status experimental

Query Match

39.0%; Score 16; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKEL 6

Db 9 LAKKI 13

Search completed: August 21, 2002, 15:30:29
Job time: 198 sec

GenCore version 4.5
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OW protein - protein search, using sw model

Run on: August 21, 2002, 15:27:31 ; Search time 23.87 Seconds
(without alignments)
65.226 Million cell updates/sec

Title: US-09-633-364-6827

Perfect score: 41

Sequence: 1 VLAKELKPV 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 2907

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SP-archae:19:
2: SP-archae:
3: SP-bacteria:
4: SP-fungi:
5: SP-human:
6: SP-invertebrate:
7: SP-mmc:
8: SP-organelle:
9: SP-phage:
10: SP-plant:
11: SP-rodent:
12: SP-virus:
13: SP-vertebrate:
14: SP-unclassified:
15: SP-virus:
16: SP-bacteriap:
17: SP-archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	61.0	11	3	Q9UR95
2	23	56.1	14	11	Q9UR05
3	19	46.3	10	10	Q9UR26
4	19	46.3	12	11	Q9UR20
5	18	43.9	12	2	Q9UR49
6	18	43.9	12	12	Q9UR49
7	17	41.5	11	8	Q9UR49
8	17	41.5	12	4	Q9UR49
9	17	41.5	12	10	Q9UR49
10	17	41.5	15	10	Q9UR49
11	16	39.0	8	4	Q9UR49
12	16	39.0	10	2	Q9UR49
13	16	39.0	10	11	Q9UR49
14	16	39.0	11	4	Q9UR49
15	16	39.0	11	4	Q9UR49
16	16	39.0	13	2	Q9UR49
17	16	39.0	13	2	Q9UR49

17	16	39.0	13	8	Q9UR49	Q9UR49
18	16	39.0	14	5	Q9UR49	Q9UR49
19	16	39.0	14	13	Q9UR49	Q9UR49
20	16	39.0	14	16	Q9UR49	Q9UR49
21	16	39.0	15	2	Q9UR49	Q9UR49
22	16	39.0	15	2	Q9UR49	Q9UR49
23	16	39.0	15	2	Q9UR49	Q9UR49
24	16	39.0	15	2	Q9UR49	Q9UR49
25	16	39.0	15	2	Q9UR49	Q9UR49
26	16	39.0	15	2	Q9UR49	Q9UR49
27	16	39.0	15	2	Q9UR49	Q9UR49
28	16	39.0	15	2	Q9UR49	Q9UR49
29	16	39.0	15	2	Q9UR49	Q9UR49
30	16	39.0	15	2	Q9UR49	Q9UR49
31	16	39.0	15	2	Q9UR49	Q9UR49
32	16	39.0	15	2	Q9UR49	Q9UR49
33	16	39.0	15	2	Q9UR49	Q9UR49
34	16	39.0	15	2	Q9UR49	Q9UR49
35	16	39.0	15	2	Q9UR49	Q9UR49
36	16	39.0	15	2	Q9UR49	Q9UR49
37	16	39.0	15	2	Q9UR49	Q9UR49
38	16	39.0	15	2	Q9UR49	Q9UR49
39	16	39.0	15	2	Q9UR49	Q9UR49
40	16	39.0	15	2	Q9UR49	Q9UR49
41	16	39.0	15	2	Q9UR49	Q9UR49
42	16	39.0	15	2	Q9UR49	Q9UR49
43	16	39.0	15	2	Q9UR49	Q9UR49
44	16	39.0	15	2	Q9UR49	Q9UR49
45	16	39.0	15	2	Q9UR49	Q9UR49

ALIGNMENTS

RESULT 1
Q9UR95 PRELIMINARY; PRT: 11 AA.
AC Q9UR95:
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE HPAT SHOCK PROTEIN 60 HOMOLOG (FRAGMENT)
OS Pichia angusta (yeast) (Hansenula polymorpha).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
CC Saccharomycetales; Saccharomycetaceae; Pichia.
CX NCBI:TaxID=4905;
RN [1]
RP
RX MEDLINE=93223840; PubMed=8096822;
RA Evers M.E., Huhse B., Tilorenko V.I., Kunau W.H., Hartl F.U.,
RA Harder W., Veenhuis M.;
RT "Affinity purification of molecular chaperones of the yeast Hansenula polymorpha using immobilized denatured alcohol oxidase";
RT FEMS Lett. 321:32-36(1993).
SQ SEQUENCE 11 AA; 1230 MW; 71872C1779C3372B CRC64;

Query Match 61.0%; Score 25; DB 3; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 KELKE 8
DB 3 KKLKE 7
RESULT 2
ID Q9UR05 PRELIMINARY; PRT: 14 AA.
AC Q9UR05:
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)

SHORTER ISOFORM OF INTERLEUKIN 15 (FRAGMENT).
 IL15 OR INTERLEUKIN 15.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=98211658; PubMed=9551932;
 RA Nishimura H., Mashizu J., Nakamura N., Enomoto A., Yoshikai Y.;
 RT "Translational efficiency is up-regulated by alternative exon in
 murine IL-15 mRNA.";
 RL J. Immunol. 160:936-942(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Prinz M., Hantsch U.K., Kettenmann H., Kirchhoff F.;
 RT "Alternative splicing of mouse IL-15 is due to the use of an internal
 splice site.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB022307; BAN37122.1;
 DR EMBL: AJ012587; CAN10069.1;
 DR MGI: 103014; 1115
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1503 MW; 62A3C388924E2B CRC64;

Query Match 56.1%; Score 23; DB 11; Length 14;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 3 AKELKFV 9
 :|||
 Db 5 SKELGFV 11

RESULT 3
 09S926 PRELIMINARY; PRT; 10 AA.
 AC 09S926;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE MONODEHYDROSCORABATE REDUCTASE II, Mrit.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolaceae; Glycine.
 NCBI_TaxID=3847;
 RX MEDLINE=92088257; PubMed=1727643;
 RA Dalton D.A., Langenberg L., Robbins M.;
 RT Purification and characterization of monodehydroascorbate reductase
 from soybean root nodules.
 RL Arch. Biochem. Biophys. 292:281-286(1992)
 SQ SEQUENCE 10 AA; 1153 MW; 848055045359D1 CRC64;

Query Match 46.3%; Score 19; DB 10; Length 10;
 Best Local Similarity 42.9%; Pred. No. 2.3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 3 AKELKFV 9
 :|||
 Db 1 AKFKFYI 7

RESULT 4
 09QZD0 PRELIMINARY; PRT; 12 AA.
 AC 09QZD0;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE SH2-CONTAINING INOSITOL PHOSPHATASE SHIP (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 RX MEDLINE=98211658; PubMed=9551932;
 RA Nishimura H., Mashizu J., Nakamura N., Enomoto A., Yoshikai Y.;
 RT "Translational efficiency is up-regulated by alternative exon in
 murine IL-15 mRNA.";
 RL J. Immunol. 160:936-942(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Prinz M., Hantsch U.K., Kettenmann H., Kirchhoff F.;
 RT "Alternative splicing of mouse IL-15 is due to the use of an internal
 splice site.";
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AB022307; BAN37122.1;
 DR EMBL: AJ012587; CAN10069.1;
 DR MGI: 103014; 1115
 FT NON_TER 14
 SQ SEQUENCE 12 AA; 1372 MW; 42F1800FB43B727 CRC64;

Query Match 46.3%; Score 19; DB 11; Length 12;
 Best Local Similarity 66.7%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLAKEL 6
 :|||
 Db 5 LLCKEL 10

RESULT 5
 09L4M9 PRELIMINARY; PRT; 12 AA.
 AC 09L4M9;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE GUANOSINE BIPHOSPHATE SYNTHETASE, PUTATIVE (FRAGMENT).
 OS REL.
 OC Streptococcus equisimilis.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
 OC Streptococcus.
 NCBI_TaxID=119602;
 RX MEDLINE=20123454; PubMed=10660058;
 RA Geyer A., Schmidt K.H.;
 RT "Genetic organisation of the m protein region in human isolates of
 group C and G streptococci: two types of multigene regulator-like
 (mgfC) regions.";
 RL Mol. Gen. Genet. 262:965-974(2000).
 DR EMBL: AJ133440; CAB70616.1;
 FT NON_TER 12
 SQ SEQUENCE 12 AA; 1334 MW; 0A82EC4258A72440 CRC64;

Query Match 43.9%; Score 18; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 4.5e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKEL 6
 :|||
 Db 1 MAKEL 5

RESULT 6
 069232 PRELIMINARY; PRT; 12 AA.
 ID 069232

AC 069232; (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE HERPESVIRUS SAIMIRI GENE 7 HOMOLOGUE (FRAGMENT).
 OS Bovine herpesvirus 4.
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Gammaherpesvirinae.
 NCBI_TaxID=10385;
 RN NCBI_TaxID=10385;
 RP SEQUENCE FROM N.A.
 RC STRAIN-V. TEST;
 RX MEDLINE=9331082; PubMed=1355698;
 RA Bublot M., Lomonte P., Leguare A.-S., Albrecht J.-C., Nicholas J.,
 RA Fleckenstein B., Pastoret P.-P., Thiry E.,
 RT "Genetic relationships between bovine herpesvirus 4 and the
 RT gammaherpesviruses Epstein-Barr virus and herpesvirus saimiri."
 RL Virology 190:654-665(1992).
 DR EMBL: M90772; AAA46019.1; -.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1338 MW; 4B800FF17ACDD07 CRC64;

Query Match 43.9%; Score 18; DB 12; Length 12;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 LAKELEY 9
 DB 1 MARLEAV 8

RESULT 7
 ID 032704 PRELIMINARY; PRT: 11 AA.
 AC 032704;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE NDHE PROTEIN (FRAGMENT).
 OS Nicotiana tabacum (Common tobacco).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; easterids I; Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID=4097;
 RN NCBI_TaxID=4097;
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRIGHT YELLOW 4; TISSUE-LEAF;
 RX MEDLINE=88210537; PubMed=3329576;
 RA Hayashida N., Matsubayashi T., Shimozaki K., Sugisura M., Inoue K.,
 RA Hayama T.,
 RT "The gene for the 9kd polypeptide, a possible apoprotein for the iron-
 RT sulfur centers A and B of the photosystem I complex in tobacco
 RT chloroplastDNA."
 RL Curr. Genet. 12:247-250(1987).
 DR EMBL: X05881; CAA29303.1; -.
 KW Chloroplast.
 FT NON_TER 1 1
 SQ SEQUENCE 11 AA; 1338 MW; 008165FE304776CB CRC64;

Query Match 41.5%; Score 17; DB 8; Length 11;
 Best Local Similarity 75.0%; Pred. No. 6.7e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 LKFV 9
 DB 7 IKFV 10

RESULT 8
 OYUNV5

ID 090NV5 PRELIMINARY; PRT: 12 AA.
 AC 090NV5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE INOSINE MONOPHOSPHATASE 2 (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN NCBI_TaxID=9606;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97463449; PubMed=9322233;
 RA Yoshikawa T., Turner G., Esterling L.E., Sanders A.R.,
 RA Detera-Wadleigh S.D.;
 RT "A novel human myo-inositol monophosphatase gene, IMP.18p, maps to a
 RT susceptibility region for bipolar disorder."
 RL Mol. Psychiatry 2:393-397(1997).
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1408 MW; D29A162A15172B06 CRC64;

Query Match 41.5%; Score 17; DB 4; Length 12;
 Best Local Similarity 60.0%; Pred. No. 7.3e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 4 KELEF 8
 DB 5 KELEF 9

RESULT 9
 ID 090QF8 PRELIMINARY; PRT: 12 AA.
 AC 090QF8;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DE CAFFEYL-COA O-METHYLTRANSFERASE (FRAGMENT).
 OS CCOCOMY.
 OS Plus taeda (loblolly pine)
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 NCBI_TaxID=3352;
 RN NCBI_TaxID=3352;
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99408257; PubMed=10480380;
 RA Li L., Osakabe Y., Joshi C.P., Chiang V.L.;
 RT "Secondary xylem-specific expression of caffeoyl-coenzyme A 3-O-
 RT methyltransferase plays an important role in the methylation pathway
 RT associated with lignin biosynthesis in loblolly pine."
 RL Plant Mol. Biol. 40:555-565(1999).
 DR EMBL: AF098159; AAF00086.1; -.
 KW Transferase; Methyltransferase.
 FT NON_TER 12 12
 SQ SEQUENCE 12 AA; 1164 MW; 8C604447E4DDC2D5 CRC64;

Query Match 41.5%; Score 17; DB 10; Length 12;
 Best Local Similarity 57.1%; Pred. No. 7.3e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0.

OY 1 VLAKELK 7
1 1 1 1
DB 6 VAAAEVK 12

RESULT 10

PRELIMINARY: PRT: 15 AA.
ID P82431;
AC P82431;
DT 01-JUN-2000 (TREMBLrel. 14, Created)
DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE 100 KDA CELL WALL PROTEIN (FRAGMENT).
OS Nicotiana glauca (Cotyledonaceae).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Aspladeae; Gesneriids I; Solanales; Solanaceae; Nicotiana.
OX NCBI_TaxId=4097;
RN [1]
RP SEQUENCE.
RC STRAIN=CV. PETIT HAVANA;
RA Bhatnagar, P., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Bhatnagar, P., Bonham V.A., Mitchell G.P.;
RA "Proteomic study of secondary cell wall proteins from transformed
tobacco culture";
RT Plants 0:0-0(2000).
CC -1 SUBCELLULAR LOCATION: CELL WALL.
CC -1 TISSUE SPECIFICITY: XYLEM.
KM CELL WALL.
FT NON_TER 15 15
SO SEQUENCE 15 AA: 1694 MW; 5F3B8D2E48187626 CRC64;

Query Match 41.8%; Score 17; DB 10; Length 15;
Best Local Similarity 57.1%; Pred. No. 8.9e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 VLAKELK 7
1 1 1 1
DB 3 VKKRDLEK 9

RESULT 11

PRELIMINARY: PRT: 8 AA.
ID 09HAD3;
AC 09HAD3;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE LIM DOMAIN ONLY 1 PROTEIN (FRAGMENT).
GN LMOL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Brueckmann T., Winterpacht A., Hankeln T., Schmidt E.R., Zabel B.U.;
RA "Human PAC clone RPCLP/04K03781 (pD7.781K3), sequenced in DHP project
(Comparative Sequencing of a 1 Mb Region in Man (Chromosome 11p15) and
Mouse (Chromosome 7))";
RT Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
RL EMBL: AJ277661; CAC14373.1;
DR NON_TER 8 8
FT SEQUENCE 8 AA: 980 MW; F3AB133AA732C696 CRC64;

Query Match 39.0%; Score 16; DB 4; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 VLAKELK 5
1 1 1 1
DB 3 VLKKE 7

RESULT 12

PRELIMINARY: PRT: 10 AA.
ID P83160;
AC P83160;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE RUBULOSE BISPHOSPHATE CARBOXYLASE SMALL CHAIN (EC 4.1.1.39) (RUBISCO
SMALL SUBUNIT) (FRAGMENT).
OS Anabaena sp. (strain L31).
OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.
OX NCBI_TaxId=29412;
RN [1]
RP SEQUENCE.
RC Apte S.K., Uhlemann E., Schmidt R., Alendort K.;
RL Submitted (OCT-2001) to the Swiss-Prot data bank.
CC -1 FUNCTION: RUBISCO CATALYZES TWO REACTIONS: THE CARBOXYLATION OF D-
RUBULOSE 1,5-BISPHOSPHATE, AND THE PRIMARY EVENT IN PHOTOSYNTHETIC
CARBON DIOXIDE FIXATION, AS WELL AS THE OXIDATIVE FRAGMENTATION OF
THE PENTOSE SUBSTRATE IN THE PHOTORESPIRATION PROCESS. BOTH
REACTIONS OCCUR SIMULTANEOUSLY AND IN COMPETITION AT THE SAME
ACTIVE SITE.
CC -1 CATALYTIC ACTIVITY: D-RUBULOSE 1,5-BISPHOSPHATE + CO(2) = 2 3-
PHOSPHO-D-GICERATE.
CC -1 PROTHO-D-GICERATE.
CC -1 CATALYTIC ACTIVITY: D-RUBULOSE 1,5-BISPHOSPHATE + O(2) = 3-
PHOSPHO-D-GICERATE + 2-PHOSPHOGLYCOLATE.
CC -1 SUBMIT: 8 LARGE CHAINS + 8 SMALL CHAINS.
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1 SIMILARITY: BELONGS TO THE RUBISCO SMALL CHAIN FAMILY.
KM Photosynthesis: Carbon dioxide fixation; Photorespiration; Lyase;
KM Photosynthetase; Monooxygenase; Calvin cycle.
FT NON_TER 10 10
SO SEQUENCE 10 AA: 1322 MW; 8B4E2D0B13276731 CRC64;

Query Match 39.0%; Score 16; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 1e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 VLAKELK 8
1 1 1 1
DB 4 LPKERRY 10

RESULT 13

PRELIMINARY: PRT: 10 AA.
ID 070580;
AC 070580;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE CARBONIC ANHYDRASE III (FRAGMENT).
GN CAR3 OR CAR5 OR CA3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Sweden J., Smith H., Morrison K., Edwards Y.;
RA "Sequence comparisons and functional studies of the proximal promoter
of the carbonic anhydrase 3 (CA3) gene";
RT Gene 214:157-165(1999).
RL EMBL: AJ006474; CAA07057.1;
DR MGD: MGI:1351477; Car3.
DR MGD: MGI:88270; Car3.
FT NON_TER 10 10
SO SEQUENCE 10 AA: 1105 MW; 567FE71ADC37B13 CRC64;

Query Match 39.0%; Score 16; DB 11; Length 10;
 Best Local Similarity 75.0%; Pred. No. 1e+04; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKE 5
 :|||
 DB 1 MAKE 4

OY 2 LAKE 5
 :|||
 DB 1 MAKE 4
 Search completed: August 21, 2002, 15:31:00
 Job time: 209 sec

RESULT 14

O9EU23 PRELIMINARY; PRT: 11 AA.
 ID O9EU23
 AC O9EU23
 DT 01-MAR-2001 (TREMBLER, 16, Created)
 DT 01-MAR-2001 (TREMBLER, 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLER, 16, Last annotation update)
 DE RIBOSOME BINDING FACTOR A (FRAGMENT).
 GN RBFA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-10490;
 RA Hedegaard J., Kristensen J.E., Nakamura Y., Sperling-Petersen H.U.,
 RT Mortensen K.K.;
 RT "Sequence of the infB gene from Escherichia coli strain 10489 and
 RT 10490.";
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDJ databases.
 DR EMBL: AJ132862; CAC20133.1; -
 FT NON_TER 11
 SO SEQUENCE 11 AA; 1319 MW; 68234CFE740879CB CRC64;

Query Match 39.0%; Score 16; DB 2; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 2 LAKE 5
 :|||
 DB 1 MAKE 4

RESULT 15

O60842 PRELIMINARY; PRT: 11 AA.
 ID O60842
 AC O60842
 DT 01-AUG-1998 (TREMBLER, 07, Created)
 DT 01-AUG-1998 (TREMBLER, 07, Last sequence update)
 DT 01-DEC-2001 (TREMBLER, 19, Last annotation update)
 DE CARBONIC ANHYDRASE (FRAGMENT).
 GN CA3.
 OS Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Sowden J., Smith H., Morrison K., Edwards Y.;
 RT "Sequence comparisons and functional studies of the proximal promoter
 RT of the carbonic anhydrase 3 (CA3) gene.";
 RL Gene 214:157-165(1999).
 DR EMBL: AJ006473; CAA07056.1; -
 FT NON_TER 11
 SO SEQUENCE 11 AA; 1293 MW; 7DB6AF84CB58637B CRC64;

Query Match 39.0%; Score 16; DB 4; Length 11;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04; 0; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;